

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (I) APPLICANT: Korenberg, Julie R.
- (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING DS-CAM
PROTEINS AND PRODUCTS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Campbell and Flores
(B) STREET: 4370 La Jolla Village Drive, Suite 700
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92122
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/029,322
(B) FILING DATE: 25-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ramos, Robert T.
(B) REGISTRATION NUMBER: 37,915
(C) REFERENCE/DOCKET NUMBER: P-CE 2817
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619-535-9001
(B) TELEFAX: 619-535-8949

(2) INFORMATION FOR SEQ ID NO:1:

- (I) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 453..6185

0895591 102390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACTGAGGC CGGAGCACGG CAAAGATGAG CCTGCCCCGCC CGCCTGCTGC CTGGATGCGG	60
AGGGTGAGGG CTGGCGCACG GGAGGCCGCT GGCTGCGCAT TCTGGGCGCC GAGTGCCCGG	120
GATGAGCTCA CGCCCGCGTC TCGGGCTCTC TCCACCTGCC GACCTGCCGG GGGCCCACTG	180
AGCTGACGGC GCACCTGGGC TCCGGCCGCA GCGTGGGGCG CGGCGCCCGG GAGCAGGTGT	240
GCAGGAGCGC AGCGCGCGGC GAGCGCAGCC CTCGCTCCGG AGCCCGGCCG CGCCGCGTGC	300
CCGGGCGGCT AGGCAGCGGC GGCGGCGGCG GCGGGCGGCG GGCGGGCGGC GGCCCCCGGG	360
CAGGTGCCGA GCGGCGAGCG GAGCCGGGCC GGGCGGAGCG CGGGGGGCGA GGCCGGCGCG	420
TCGCTCGCGG GAGGCCGGGG AGCGGCAGGG GC ATG TGG ATA CTG GCT CTC TCC	473
Met Trp Ile Leu Ala Leu Ser	
1 5	
TTG TTC CAG AGC TTC GCG AAT GTT TTC AGT GAA GAC CTA CAC TCC AGC	521
Leu Phe Gln Ser Phe Ala Asn Val Phe Ser Glu Asp Leu His Ser Ser	
10 15 20	
CTC TAC TTT GTC AAT GCA TCT CTG CAA GAG GTA GTG TTT GCC AGC ACC	569
Leu Tyr Phe Val Asn Ala Ser Leu Gln Glu Val Val Phe Ala Ser Thr	
25 30 35	
ACG GGG ACT CTG GTG CCC TGC CCC GCA GCA GGC ATC CCT CCT GTG ACT	617
Thr Gly Thr Leu Val Pro Cys Pro Ala Ala Gly Ile Pro Pro Val Thr	
40 45 50 55	
CTC AGA TGG TAC CTA GCC ACG GGC GAG GAG ATC TAC GAT GTC CCC GGG	665
Leu Arg Trp Tyr Leu Ala Thr Gly Glu Glu Ile Tyr Asp Val Pro Gly	
60 65 70	
ATC CGC CAC GTC CAC CCC AAC GGC ACT CTC CAA ATT TTC CCC TTC CCT	713
Ile Arg His Val His Pro Asn Gly Thr Leu Gln Ile Phe Pro Phe Pro	
75 80 85	
CCT TCA AGC TTC AGT ACC TTA ATC CAT GAT AAT ACT TAT TAT TGC ACA	761
Pro Ser Ser Phe Ser Thr Leu Ile His Asp Asn Thr Tyr Tyr Cys Thr	
90 95 100	
GCT GAA AAT CCT TCA GGG AAA ATT AGA AGT CAG GAT GTC CAC ATC AAG	809
Ala Glu Asn Pro Ser Gly Lys Ile Arg Ser Gln Asp Val His Ile Lys	
105 110 115	
GCT GTT TTA CGG GAG CCC TAT ACA GTC CGT GTG GAG GAC CAG AAA ACC	857
Ala Val Leu Arg Glu Pro Tyr Thr Val Arg Val Glu Asp Gln Lys Thr	
120 125 130 135	
ATG AGA GGC AAT GTT GCG GTC TTC AAG TGC ATT ATC CCC TCC TCG GTG	905
Met Arg Gly Asn Val Ala Val Phe Lys Cys Ile Ile Pro Ser Ser Val	
140 145 150	
GAG GCG TAC ATC ACT GTC GTC TCA TGG GAG AAA GAC ACT GTT TCA CTT	953
Glu Ala Tyr Ile Thr Val Val Ser Trp Glu Lys Asp Thr Val Ser Leu	
155 160 165	
GTC TCA GGA TCT AGA TTT CTC ATC ACA TCC ACG GGA GCC TTG TAT ATT	1001
Val Ser Gly Ser Arg Phe Leu Ile Thr Ser Thr Gly Ala Leu Tyr Ile	
170 175 180	

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AAA Lys	GAT Asp	GTA Val	CAG Gln	AAT Asn	GAA Glu	GAT Asp	GGA Gly	TTG Leu	TAT Tyr	AAC Asn	TAC Tyr	CGC Arg	TGC Cys	ATC Ile	ACG Thr	1049
185						190					195					
CGG Arg	CAT His	CGA Arg	TAC Tyr	ACC Thr	GGA Gly	GAG Glu	ACG Thr	AGG Arg	CAG Gln	AGC Ser	AAC Asn	AGC Ser	GCC Ala	AGA Arg	CTT Leu	1097
200					205					210					215	
TTT Phe	GTA Val	TCA Ser	GAC Asp	CCA Pro	GCG Ala	AAC Asn	TCA Ser	GCC Ala	CCA Pro	TCC Ser	ATA Ile	CTG Leu	GAT Asp	GGG Gly	TTT Phe	1145
				220					225					230		
GAC Asp	CAT His	CGC Arg	AAA Lys	GCC Ala	ATG Met	GCT Ala	GGG Gly	CAG Gln	CGT Arg	GTG Val	GAG Glu	CTG Leu	CCT Pro	TGC Cys	AAA Lys	1193
			235					240					245			
GCG Ala	CTC Leu	GGG Gly	CAC His	CCT Pro	GAG Glu	CCA Pro	GAT Asp	TAC Tyr	CGC Arg	TGG Trp	CTG Leu	AAG Lys	GAC Asp	AAC Asn	ATG Met	1241
		250					255					260				
CCC Pro	CTG Leu	GAA Glu	CTT Leu	TCA Ser	GGG Gly	AGG Arg	TTC Phe	CAG Gln	AAG Lys	ACC Thr	GTG Val	ACG Thr	GGG Gly	CTG Leu	CTC Leu	1289
		265				270					275					
ATT Ile	GAG Glu	AAC Asn	ATT Ile	CGC Arg	CCC Pro	TCG Ser	GAC Asp	TCA Ser	GGC Gly	AGC Ser	TAT Tyr	GTT Val	TGT Cys	GAA Glu	GTG Val	1337
					285					290					295	
TCC Ser	AAC Asn	AGA Arg	TAC Tyr	GGA Gly	ACT Thr	GCT Ala	AAG Lys	GTG Val	ATA Ile	GGC Gly	CGC Arg	CTG Leu	TAC Tyr	GTG Val	AAA Lys	1385
				300					305					310		
CAG Gln	CCA Pro	CTG Leu	AAA Lys	GCC Ala	ACC Thr	ATC Ile	AGT Ser	CCC Pro	AGG Arg	AAG Lys	GTT Val	AAA Lys	AGC Ser	AGC Ser	GTG Val	1433
			315					320					325			
GGT Gly	AGC Ser	CAA Gln	GTT Val	TCC Ser	TTG Leu	TCC Ser	TGC Cys	AGC Ser	GTG Val	ACA Thr	GGA Gly	ACT Thr	GAG Glu	GAC Asp	CAG Gln	1481
		330					335					340				
GAA Glu	CTC Leu	TCC Ser	TGG Trp	TAC Tyr	CGC Arg	AAT Asn	GGT Gly	GAA Glu	ATC Ile	CTC Leu	AAC Asn	CCT Pro	GGA Gly	AAA Lys	AAT Asn	1529
		345				350					355					
GTG Val	AGG Arg	ATC Ile	ACA Thr	GGG Gly	ATC Ile	AAC Asn	CAC His	GAA Glu	AAC Asn	CTT Leu	ATA Ile	ATG Met	GAT Asp	CAC His	ATG Met	1577
					365					370					375	
GTC Val	AAA Lys	AGT Ser	GAC Asp	GGG Gly	GGC Gly	GCA Ala	TAC Tyr	CAG Gln	TGC Cys	TTT Phe	GTG Val	CGC Arg	AAG Lys	GAC Asp	AAG Lys	1625
				380					385					390		
CTG Leu	TCC Ser	GCT Ala	CAA Gln	GAC Asp	TAT Tyr	GTG Val	CAG Gln	GTG Val	GTC Val	CTT Leu	GAA Glu	GAT Asp	GGA Gly	ACT Thr	CCC Pro	1673
			395					400					405			
AAA Lys	ATT Ile	ATT Ile	TCT Ser	GCC Ala	TTT Phe	AGT Ser	GAA Glu	AAG Lys	GTG Val	GTG Val	AGT Ser	CCA Pro	GCA Ala	GAG Glu	CCG Pro	1721
			410				415					420				
GTT Val	TCC Ser	CTT Leu	ATG Met	TGC Cys	AAC Asn	GTG Val	AAG Lys	GGA Gly	ACA Thr	CCT Pro	TTG Leu	CCC Pro	ACG Thr	ATC Ile	ACG Thr	1769
		425				430					435					

TGG	ACC	CTG	GAC	GAT	GAC	CCG	ATT	CTC	AAG	GGT	GGC	AGT	CAC	CGC	ATC	1817
Trp	Thr	Leu	Asp	Asp	Asp	Pro	Ile	Leu	Lys	Gly	Gly	Ser	His	Arg	Ile	
440					445					450					455	
AGC	CAG	ATG	ATC	ACG	TCG	GAG	GGG	AAC	GTG	GTC	AGC	TAC	CTG	AAC	ATC	1865
Ser	Gln	Met	Ile	Thr	Ser	Glu	Gly	Asn	Val	Val	Ser	Tyr	Leu	Asn	Ile	
				460					465						470	
TCC	AGC	TCC	CAG	GTC	CGG	GAC	GGG	GGA	GTC	TAC	CGC	TGC	ACT	GCC	AAC	1913
Ser	Ser	Ser	Gln	Val	Arg	Asp	Gly	Gly	Val	Tyr	Arg	Cys	Thr	Ala	Asn	
			475					480					485			
AAC	TCG	GCG	GGA	GTC	GTC	CTG	TAC	CAG	GCT	CGA	ATA	AAC	GTA	AGA	GGG	1961
Asn	Ser	Ala	Gly	Val	Val	Leu	Tyr	Gln	Ala	Arg	Ile	Asn	Val	Arg	Gly	
		490					495					500				
CCT	GCA	AGC	ATT	CGA	CCA	ATG	AAA	AAC	ATC	ACA	GCA	ATA	GCA	GGA	CGG	2009
Pro	Ala	Ser	Ile	Arg	Pro	Met	Lys	Asn	Ile	Thr	Ala	Ile	Ala	Gly	Arg	
	505					510					515					
GAC	ACA	TAC	ATT	CAC	TGT	CGT	GTG	ATT	GGC	TAT	CCG	TAT	TAC	TCC	ATT	2057
Asp	Thr	Tyr	Ile	His	Cys	Arg	Val	Ile	Gly	Tyr	Pro	Tyr	Tyr	Ser	Ile	
520					525					530					535	
AAA	TGG	TAC	AAG	AAC	TCT	AAC	CTG	CTT	CCT	TTC	AAC	CAC	CGC	CAA	GTG	2105
Lys	Trp	Tyr	Lys	Asn	Ser	Asn	Leu	Leu	Pro	Phe	Asn	His	Arg	Gln	Val	
				540					545					550		
GCA	TTT	GAG	AAC	AAT	GGA	ACT	CTT	AAA	CTT	TCA	GAT	GTG	CAA	AAG	GAA	2153
Ala	Phe	Glu	Asn	Asn	Gly	Thr	Leu	Lys	Leu	Ser	Asp	Val	Gln	Lys	Glu	
			555					560					565			
GTG	GAC	GAG	GGG	GAG	TAC	ACG	TGC	AAC	GTG	TTG	GTT	CAA	CCA	CAA	CTC	2201
Val	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Asn	Val	Leu	Val	Gln	Pro	Gln	Leu	
	570						575					580				
TCC	ACC	AGC	CAG	AGC	GTC	CAC	GTG	ACC	GTG	AAA	GTT	CCG	CCT	TTC	ATA	2249
Ser	Thr	Ser	Gln	Ser	Val	His	Val	Thr	Val	Lys	Val	Pro	Pro	Phe	Ile	
	585					590					595					
CAA	CCC	TTT	GAG	TTT	CCA	AGA	TTC	TCC	ATT	GGG	CAG	CGG	GTC	TTC	ATC	2297
Gln	Pro	Phe	Glu	Phe	Pro	Arg	Phe	Ser	Ile	Gly	Gln	Arg	Val	Phe	Ile	
600					605					610					615	
CCC	TGT	GTT	GTG	GTC	TCA	GGG	GAC	TTA	CCC	ATC	ACG	ATC	ACC	TGG	CAG	2345
Pro	Cys	Val	Val	Val	Ser	Gly	Asp	Leu	Pro	Ile	Thr	Ile	Thr	Trp	Gln	
				620					625					630		
AAG	GAT	GGC	CGG	CCA	ATC	CCT	GGG	AGC	CTT	GGG	GTG	ACC	ATT	GAC	AAT	2393
Lys	Asp	Gly	Arg	Pro	Ile	Pro	Gly	Ser	Leu	Gly	Val	Thr	Ile	Asp	Asn	
			635					640					645			
ATT	GAC	TTC	ACG	AGC	TCC	TTG	AGG	ATT	TCC	AAT	CTC	TCG	CTC	ATG	CAC	2441
Ile	Asp	Phe	Thr	Ser	Ser	Leu	Arg	Ile	Ser	Asn	Leu	Ser	Leu	Met	His	
		650					655					660				
AAT	GGG	AAT	TAC	ACC	TGC	ATA	GCC	CGG	AAT	GAG	GCC	GCC	GCT	GTG	GAG	2489
Asn	Gly	Asn	Tyr	Thr	Cys	Ile	Ala	Arg	Asn	Glu	Ala	Ala	Ala	Val	Glu	
	665					670					675					
CAC	CAA	AGC	CAG	TTG	ATT	GTC	AGA	GTT	CCT	CCC	AAG	TTT	GTG	GTT	CAG	2537
His	Gln	Ser	Gln	Leu	Ile	Val	Arg	Val	Pro	Pro	Lys	Phe	Val	Val	Gln	
680					685					690					695	

CCA Pro	CGG Arg	GAC Asp	CAG Gln	GAC Asp 700	GGG Gly	ATT Ile	TAT Tyr	GGC Gly	AAA Lys 705	GCA Ala	GTC Val	ATC Ile	CTC Leu	AAT Asn 710	TGT Cys	2585
TCT Ser	GCT Ala	GAG Glu	GGT Gly 715	TAC Tyr	CCT Pro	GTA Val	CCT Pro	ACC Thr 720	ATC Ile	GTG Val	TGG Trp	AAA Lys	TTC Phe 725	TCT Ser	AAA Lys	2633
GGT Gly	GCT Ala	GGG Gly 730	GTT Val	CCC Pro	CAG Gln	TTC Phe	CAG Gln 735	CCA Pro	ATT Ile	GCC Ala	CTA Leu	AAT Asn 740	GGC Gly	CGA Arg	ATC Ile	2681
CAA Gln	GTT Val 745	CTC Leu	AGC Ser	AAT Asn	GGG Gly	TCG Ser 750	TTG Leu	CTG Leu	ATC Ile	AAG Lys	CAT His 755	GTC Val	GTG Val	GAG Glu	GAA Glu	2729
GAC Asp 760	AGT Ser	GGC Gly	TAC Tyr	TAC Tyr	CTC Leu 765	TGC Cys	AAG Lys	GTC Val	AGC Ser	AAC Asn 770	GAT Asp	GTG Val	GGC Gly	GCA Ala	GAC Asp 775	2777
GTC Val	AGC Ser	AAG Lys	TCC Ser	ATG Met 780	TAC Tyr	CTC Leu	ACG Thr	GTT Val	AAA Lys 785	ATT Ile	CCT Pro	GCG Ala	ATG Met 790	ATA Ile	ACA Thr	2825
TCC Ser	TAT Tyr	CCA Pro	AAT Asn 795	ACT Thr	ACC Thr	CTG Leu	GCC Ala	ACG Thr 800	CAG Gln	GGG Gly	CAG Gln	AAA Lys	AAG Lys 805	GAG Glu	ATG Met	2873
AGC Ser	TGC Cys	ACG Thr 810	GCG Ala	CAT His	GGT Gly	GAG Glu	AAG Lys 815	CCC Pro	ATT Ile	ATA Ile	GTC Val	CGC Arg 820	TGG Trp	GAG Glu	AAG Lys	2921
GAG Glu 825	GAC Asp	CGA Arg	ATC Ile	ATT Ile	AAC Asn	CCT Pro 830	GAG Glu	ATG Met	GCC Ala	CGT Arg	TAT Tyr 835	CTT Leu	GTG Val	TCC Ser	ACC Thr	2969
AAG Lys 840	GAG Glu	GTG Val	GGA Gly	GAA Glu	GAG Glu 845	GTG Val	ATT Ile	TCT Ser	ACT Thr	CTG Leu 850	CAG Gln	ATT Ile	TTG Leu	CCA Pro	ACT Thr 855	3017
GTG Val	AGA Arg	GAA Glu	GAT Asp	TCT Ser 860	GGT Gly	TTC Phe	TTT Phe	TCC Ser	TGC Cys 865	CAT His	GCT Ala	ATT Ile	AAT Asn	TCT Ser 870	TAT Tyr	3065
GGG Gly	GAG Glu	GAC Asp	CGT Arg 875	GGA Gly	ATA Ile	ATT Ile	CAG Gln	CTC Leu 880	ACA Thr	GTG Val	CAA Gln	GAG Glu	CCC Pro 885	CCA Pro	GAC Asp	3113
CCT Pro	CCC Pro	GAA Glu 890	ATT Ile	GAG Glu	ATC Ile	AAA Lys	GAT Asp 895	GTC Val	AAA Lys	GCA Ala	CGC Arg	ACA Thr 900	ATT Ile	ACG Thr	CTC Leu	3161
AGG Arg	TGG Trp 905	ACC Thr	ATG Met	GGG Gly	TTT Phe	GAT Asp 910	GGA Gly	AAC Asn	AGT Ser	CCC Pro	ATC Ile 915	ACA Thr	GGC Gly	TAC Tyr	GAT Asp	3209
ATT Ile 920	GAA Glu	TGC Cys	AAA Lys	AAT Asn	AAA Lys 925	TCA Ser	GAC Asp	TCC Ser	TGG Trp	GAT Asp 930	TCT Ser	GCT Ala	CAG Gln	AGA Arg	ACC Thr 935	3257
AAA Lys	GAT Asp	GTT Val	TCC Ser	CCT Pro 940	CAG Gln	CTG Leu	AAC Asn	TCG Ser	GCC Ala 945	ACC Thr	ATC Ile	ATT Ile	GAT Asp 950	ATC Ile	CAC His	3305

CCT Pro	TCC Ser	TCC Ser	ACC Thr 955	TAC Tyr	AGC Ser	ATC Ile	CGC Arg	ATG Met 960	TAC Tyr	GCC Ala	AAG Lys	AAC Asn	CGG Arg 965	ATT Ile	GGC Gly	3353
AAG Lys	AGC Ser	GAG Glu 970	CCC Pro	AGC Ser	AAC Asn	GAG Glu	CTC Leu 975	ACC Thr	ATC Ile	ACG Thr	GCG Ala	GAC Asp 980	GAG Glu	GCA Ala	GCT Ala	3401
CCT Pro	GAT Asp 985	GGT Gly	CCA Pro	CCT Pro	CAG Gln	GAA Glu 990	GTT Val	CAC His	CTG Leu	GAG Glu	CCT Pro 995	ATA Ile	TCA Ser	TCT Ser	CAG Gln	3449
AGC Ser 1000	ATC Ile	AGG Arg	GTC Val	ACA Thr	TGG Trp 1005	AAG Lys	GCT Ala	CCC Pro	AAG Lys	AAA Lys 1010	CAT His	TTG Leu	CAA Gln	AAT Asn	GGG Gly 1015	3497
ATT Ile	ATC Ile	CGT Arg	GGC Gly	TAC Tyr 1020	CAA Gln	ATA Ile	GGT Gly	TAC Tyr	CGA Arg 1025	GAG Glu	TAC Tyr	AGC Ser	ACT Thr	GGG Gly 1030	GGT Gly	3545
AAC Asn	TTC Phe	CAA Gln 1035	TTC Phe	AAC Asn	ATT Ile	ATC Ile	AGT Ser 1040	GTC Val	GAC Asp	ACC Thr	AGC Ser	GGG Gly 1045	GAC Asp	AGT Ser	GAG Glu	3593
GTT Val	TAC Tyr	ACC Thr 1050	CTG Leu	GAC Asp	AAC Asn	CTG Leu	AAT Asn 1055	AAG Lys	TTC Phe	ACT Thr	CAG Gln	TAC Tyr 1060	GGC Gly	CTG Leu	GTG Val	3641
GTG Val	CAG Gln 1065	GCC Ala	TGT Cys	AAC Asn	CGG Arg	GCC Ala 1070	GGC Gly	ACG Thr	GGG Gly	CCT Pro	TCT Ser 1075	TCT Ser	CAG Gln	GAA Glu	ATC Ile	3689
ATC Ile 1080	ACC Thr	ACC Thr	ACT Thr	CTC Leu	GAG Glu 1085	GAT Asp	GTG Val	CCC Pro	AGT Ser	TAC Tyr 1090	CCC Pro	CCC Pro	GAA Glu	AAT Asn	GTC Val 1095	3737
CAA Gln	GCC Ala	ATA Ile	GCA Ala 1100	ACA Thr	TCA Ser	CCA Pro	GAA Glu	AGC Ser	ATA Ile 1105	TCA Ser	ATA Ile	TCC Ser	TGG Trp	TCC Ser 1110	ACA Thr	3785
CTT Leu	TCC Ser	AAG Lys	GAA Glu 1115	GCC Ala	TTG Leu	AAT Asn	GGA Gly	ATT Ile 1120	CTC Leu	CAG Gln	GGG Gly	TTC Phe	AGA Arg 1125	GTC Val	ATT Ile	3833
TAC Tyr	TGG Trp	GCC Ala 1130	AAC Asn	CTC Leu	ATG Met	GAC Asp	GGA Gly 1135	GAG Glu	CTG Leu	GGT Gly	GAG Glu	ATT Ile 1140	AAA Lys	AAC Asn	ATC Ile	3881
ACC Thr	ACC Thr 1145	ACA Thr	CAG Gln	CCT Pro	TCA Ser	CTG Leu 1150	GAG Glu	CTG Leu	GAC Asp	GGG Gly	CTG Leu 1155	GAA Glu	AAG Lys	TAC Tyr	ACC Thr	3929
AAC Asn 1160	TAC Tyr	AGC Ser	ATC Ile	CAG Gln	GTG Val 1165	CTG Leu	GCC Ala	TTC Phe	ACC Thr	CGC Arg 1170	GCA Ala	GGA Gly	GAC Asp	GGG Gly	GTC Val 1175	3977
AGG Arg	AGT Ser	GAG Glu	CAG Gln	ATC Ile 1180	TTC Phe	ACC Thr	CGG Arg	ACC Thr	AAA Lys 1185	GAG Glu	GAT Asp	GTT Val	CCA Pro	GGT Gly 1190	CCT Pro	4025
CCC Pro	GCG Ala	GGT Gly	GTG Val 1195	AAG Lys	GCA Ala	GCG Ala	GCG Ala	GCC Ala 1200	TCA Ser	GCC Ala	TCC Ser	ATG Met 1205	GTC Val	TTT Phe	GTG Val	4073

TCC TGG CTT CCC CCT CTC AAG CTG AAC GGC ATC ATC CGA AAG TAC ACT	4121
Ser Trp Leu Pro Pro Leu Lys Leu Asn Gly Ile Ile Arg Lys Tyr Thr	
1210 1215 1220	
GTA TTC TGC TCC CAC CCC TAT CCC ACA GTG ATC AGC GAG TTT GAG GCC	4169
Val Phe Cys Ser His Pro Tyr Pro Thr Val Ile Ser Glu Phe Glu Ala	
1225 1230 1235	
TCT CCC GAC TCG TTT TCC TAC AGA ATT CCC AAC CTG AGT AGG AAT CGT	4217
Ser Pro Asp Ser Phe Ser Tyr Arg Ile Pro Asn Leu Ser Arg Asn Arg	
1240 1245 1250 1255	
CAG TAC AGC GTC TGG GTG GTG GCT GTT ACT TCA GCC GGA AGA GGC AAC	4265
Gln Tyr Ser Val Trp Val Val Ala Val Thr Ser Ala Gly Arg Gly Asn	
1260 1265 1270	
AGC AGT GAA ATC ATC ACA GTC GAG CCA CTA GCA AAA GCT CCT GCA CGA	4313
Ser Ser Glu Ile Ile Thr Val Glu Pro Leu Ala Lys Ala Pro Ala Arg	
1275 1280 1285	
ATC CTG ACC TTC AGT GGG ACA GTG ACT ACT CCA TGG ATG AAA GAC ATT	4361
Ile Leu Thr Phe Ser Gly Thr Val Thr Thr Pro Trp Met Lys Asp Ile	
1290 1295 1300	
GTC TTG CCT TGT AAG GCT GTT GGG GAC CCT TCT CCT GCA GTC AAA TGG	4409
Val Leu Pro Cys Lys Ala Val Gly Asp Pro Ser Pro Ala Val Lys Trp	
1305 1310 1315	
ATG AAA GAC AGT AAC GGG ACA CCC AGT CTA GTA ACG ATT GAT GGG CGG	4457
Met Lys Asp Ser Asn Gly Thr Pro Ser Leu Val Thr Ile Asp Gly Arg	
1320 1325 1330 1335	
AGG AGC ATC TTT AGC AAC GGA AGC TTC ATT ATT CGC ACG GTG AAA GCA	4505
Arg Ser Ile Phe Ser Asn Gly Ser Phe Ile Ile Arg Thr Val Lys Ala	
1340 1345 1350	
GAA GAC TCC GGC TAT TAC AGC TGC ATT GCC AAT AAC AAC TGG GGA TCT	4553
Glu Asp Ser Gly Tyr Tyr Ser Cys Ile Ala Asn Asn Asn Trp Gly Ser	
1355 1360 1365	
GAT GAA ATT ATT TTA AAC TTA CAA GTA CAA GTT CCA CCA GAT CAG CCT	4601
Asp Glu Ile Ile Leu Asn Leu Gln Val Gln Val Pro Pro Asp Gln Pro	
1370 1375 1380	
CGG CTT ACA GTC TCC AAG ACC ACG TCT TCC TCC ATC ACC CTT TCT TGG	4649
Arg Leu Thr Val Ser Lys Thr Thr Ser Ser Ser Ile Thr Leu Ser Trp	
1385 1390 1395	
CTC CCT GGA GAC AAC GGG GGC AGC TCT ATC AGA GGA TAC ATA CTG CAG	4697
Leu Pro Gly Asp Asn Gly Gly Ser Ser Ile Arg Gly Tyr Ile Leu Gln	
1400 1405 1410 1415	
TAC TCC GAG GAC AAT AGT GAG CAG TGG GGG AGT TTT CCA ATC AGC CCC	4745
Tyr Ser Glu Asp Asn Ser Glu Gln Trp Gly Ser Phe Pro Ile Ser Pro	
1420 1425 1430	
AGC GAA CGT TCC TAT CGC TTG GAA AAT CTC AAA TGT GGG ACT TGG TAT	4793
Ser Glu Arg Ser Tyr Arg Leu Glu Asn Leu Lys Cys Gly Thr Trp Tyr	
1435 1440 1445	
AAG TTC ACA CTG ACA GCC CAA AAT GGA GTG GGC CCA GGG CGC ATA AGT	4841
Lys Phe Thr Leu Thr Ala Gln Asn Gly Val Gly Pro Gly Arg Ile Ser	
1450 1455 1460	

00906591 00906591

GAA ATC ATA GAA GCA AAG ACC TTA GGA AAA GAG CCC CAG TTC TCA AAG Glu Ile Ile Glu Ala Lys Thr Leu Gly Lys Glu Pro Gln Phe Ser Lys 1465 1470 1475	4889
GAG CAG GAG CTG TTT GCC AGC ATC AAC ACC ACA CGC GTG AGG CTG AAC Glu Gln Glu Leu Phe Ala Ser Ile Asn Thr Thr Arg Val Arg Leu Asn 1480 1485 1490 1495	4937
CTC ATT GGC TGG AAT GAT GGC GGC TGC CCC ATC ACC TCC TTC ACA CTA Leu Ile Gly Trp Asn Asp Gly Gly Cys Pro Ile Thr Ser Phe Thr Leu 1500 1505 1510	4985
GAG TAC AGG CCC TTT GGG ACC ACA GTT TGG ACC ACA GCT CAG AGG ACC Glu Tyr Arg Pro Phe Gly Thr Thr Val Trp Thr Thr Ala Gln Arg Thr 1515 1520 1525	5033
TCT CTC TCC AAG TCC TAC ATC CTG TAT GAC CTG CAG GAA GCC ACC TGG Ser Leu Ser Lys Ser Tyr Ile Leu Tyr Asp Leu Gln Glu Ala Thr Trp 1530 1535 1540	5081
TAT GAG CTG CAG ATG CGG GTG TGC AAC AGT GCG GGC TGC GCG GAG AAG Tyr Glu Leu Gln Met Arg Val Cys Asn Ser Ala Gly Cys Ala Glu Lys 1545 1550 1555	5129
CAG GCC AAC TTC GCT ACG CTG AAC TAC GAT GGC AGT ACA ATT CCT CCA Gln Ala Asn Phe Ala Thr Leu Asn Tyr Asp Gly Ser Thr Ile Pro Pro 1560 1565 1570 1575	5177
CTC ATT AAG TCA GTT GTC CAA AAC GAA GAA GGG CTG ACG ACC AAC GAG Leu Ile Lys Ser Val Val Gln Asn Glu Glu Gly Leu Thr Thr Asn Glu 1580 1585 1590	5225
GGG CTC AAG ATG CTG GTG ACC ATC TCC TGT ATC CTG GTG GGG GTC TTG Gly Leu Lys Met Leu Val Thr Ile Ser Cys Ile Leu Val Gly Val Leu 1595 1600 1605	5273
CTG CTG TTT GTG CTC CTG CTG GTT GTG CGG AGG AGG CGG CGG GAG CAG Leu Leu Phe Val Leu Leu Leu Val Val Arg Arg Arg Arg Arg Glu Gln 1610 1615 1620	5321
AGG CTA AAG AGG CTG CGA GAT GCA AAG AGT TTA GCT GAA ATG CTC ATG Arg Leu Lys Arg Leu Arg Asp Ala Lys Ser Leu Ala Glu Met Leu Met 1625 1630 1635	5369
AGT AAG AAT ACC CGG ACT TCA GAT ACG TTA AGC AAG CAA CAG CAG ACC Ser Lys Asn Thr Arg Thr Ser Asp Thr Leu Ser Lys Gln Gln Gln Thr 1640 1645 1650 1655	5417
CTG CGA ATG CAC ATC GAC ATA CCC AGG GCT CAG CTT TTG ATT GAA GAG Leu Arg Met His Ile Asp Ile Pro Arg Ala Gln Leu Leu Ile Glu Glu 1660 1665 1670	5465
AGA GAC ACG ATG GAG ACC ATT GAT GAT CGC TCC ACG GTT CTG TTG ACG Arg Asp Thr Met Glu Thr Ile Asp Asp Arg Ser Thr Val Leu Leu Thr 1675 1680 1685	5513
GAT GCT GAC TTT GGA GAG GCA GCT AAG CAG AAG TCC CTG ACG GTC ACT Asp Ala Asp Phe Gly Glu Ala Ala Lys Gln Lys Ser Leu Thr Val Thr 1690 1695 1700	5561
CAC ACG GTC CAT TAC CAA TCG GTG TCT CAG GCC ACT GGG CCC TTA GTG His Thr Val His Tyr Gln Ser Val Ser Gln Ala Thr Gly Pro Leu Val 1705 1710 1715	5609

GAT GTT TCA GAC GCT CGG CCG GGA ACG AAT CCC ACC ACC AGG AGG AAT Asp Val Ser Asp Ala Arg Pro Gly Thr Asn Pro Thr Thr Arg Arg Asn 1720 1725 1730 1735	5657
GCC AAG GCT GGG CCC ACA GCG AGA AAC CGC TAT GCC AGC CAG TGG ACC Ala Lys Ala Gly Pro Thr Ala Arg Asn Arg Tyr Ala Ser Gln Trp Thr 1740 1745 1750	5705
CTC AAC CGA CCC CAC CCC ACC ATC TCA GCA CAC ACC CTC ACC ACA GAC Leu Asn Arg Pro His Pro Thr Ile Ser Ala His Thr Leu Thr Thr Asp 1755 1760 1765	5753
TGG AGG CTG CCA ACA CCC AGG GCT GCA GGA TCA GTA GAC AAA GAG AGC Trp Arg Leu Pro Thr Pro Arg Ala Ala Gly Ser Val Asp Lys Glu Ser 1770 1775 1780	5801
GAC AGT TAC AGC GTC AGC CCC TCG CAA GAC ACA GAT CGA GCA AGA AGC Asp Ser Tyr Ser Val Ser Pro Ser Gln Asp Thr Asp Arg Ala Arg Ser 1785 1790 1795	5849
AGC ATG GTC TCC ACA GAA AGT GCC TCC TCC ACT TAC GAA GAA CTG GCC Ser Met Val Ser Thr Glu Ser Ala Ser Ser Thr Tyr Glu Glu Leu Ala 1800 1805 1810 1815	5897
AGG GCC TAC GAA CAC GCC AAG ATG GAA GAG CAA CTG AGG CAC GCC AAG Arg Ala Tyr Glu His Ala Lys Met Glu Glu Gln Leu Arg His Ala Lys 1820 1825 1830	5945
TTC ACC ATC ACG GAG TGC TTC ATA TCA GAC ACG TCA TCG GAG CAG TTG Phe Thr Ile Thr Glu Cys Phe Ile Ser Asp Thr Ser Ser Glu Gln Leu 1835 1840 1845	5993
ACG GCA GGG ACA AAT GAG TAC ACG GAC AGT CTG ACC TCC AGC ACC CCT Thr Ala Gly Thr Asn Glu Tyr Thr Asp Ser Ser Leu Thr Ser Ser Thr Pro 1850 1855 1860	6041
TCC GAA TCG GGA ATC TGC AGG TTC ACT GCA TCT CCC CCC AAA CCT CAG Ser Glu Ser Gly Ile Cys Arg Phe Thr Ala Ser Pro Pro Lys Pro Gln 1865 1870 1875	6089
GAT GGA GGA AGA GTA ATG AAT ATG GCA GTT CCA AAG GCA ATC GGC CAG Asp Gly Gly Arg Val Met Asn Met Ala Val Pro Lys Ala Ile Gly Gln 1880 1885 1890 1895	6137
GTG ACC TCA TAC ATT TGC CTC CAT ACC TTA GAA TGG ACT TTT TGT TAAACCGAGG Val Thr Ser Tyr Ile Cys Leu His Thr Leu Glu Trp Thr Phe Cys 1900 1905 1910	
TGGTCCAGGC ACCAGCAGGG ACCTGAGCTT AGGACAAGCA TGCTTGGAAC CTCAGAAAAG	6252
CCGGACCCTG AAGCGCCCCA CGGTCCTGGA GCCCATCCCG ATGGAAGCCG CCTCCTCCGC	6312
CTCCTCCACG AGAGAAGGAC AGTCGTGGCA GCCGGGGGCC GTGGCCACAT TACCTCAGCG	6372
GGAGGGAGCA GAGCTGGGAC AGGCAGCTAA AATGAGCAGC TCCCAAGAAT CACTGCTCGA	6432
CTCCCGGGGC CATTTGAAAG GAAACAATCC TTACGCAAAA TCTTACACCC TGGTATAACA	6492
GACAGCATGA CTGGACAGCG GTTGTAATA CAATTCAAAC AATTCAATCA AAGCTACCTT	6552
TTTTTTACGG AATTCCAATA TTTATAATTA AAGAAAATTG CCAAAATATA TT	6604

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1910 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Trp	Ile	Leu	Ala 5	Leu	Ser	Leu	Phe	Gln 10	Ser	Phe	Ala	Asn	Val 15	Phe
Ser	Glu	Asp	Leu 20	His	Ser	Ser	Leu	Tyr 25	Phe	Val	Asn	Ala	Ser 30	Leu	Gln
Glu	Val	Val 35	Phe	Ala	Ser	Thr	Thr 40	Gly	Thr	Leu	Val	Pro 45	Cys	Pro	Ala
Ala	Gly 50	Ile	Pro	Pro	Val	Thr 55	Leu	Arg	Trp	Tyr	Leu 60	Ala	Thr	Gly	Glu
Glu 65	Ile	Tyr	Asp	Val	Pro 70	Gly	Ile	Arg	His	Val 75	His	Pro	Asn	Gly	Thr 80
Leu	Gln	Ile	Phe	Pro 85	Phe	Pro	Pro	Ser	Ser 90	Phe	Ser	Thr	Leu	Ile 95	His
Asp	Asn	Thr	Tyr 100	Tyr	Cys	Thr	Ala	Glu 105	Asn	Pro	Ser	Gly	Lys 110	Ile	Arg
Ser	Gln	Asp 115	Val	His	Ile	Lys	Ala 120	Val	Leu	Arg	Glu	Pro 125	Tyr	Thr	Val
Arg	Val 130	Glu	Asp	Gln	Lys	Thr 135	Met	Arg	Gly	Asn	Val 140	Ala	Val	Phe	Lys
Cys 145	Ile	Ile	Pro	Ser	Ser 150	Val	Glu	Ala	Tyr	Ile 155	Thr	Val	Val	Ser	Trp 160
Glu	Lys	Asp	Thr	Val 165	Ser	Leu	Val	Ser	Gly 170	Ser	Arg	Phe	Leu	Ile 175	Thr
Ser	Thr	Gly	Ala 180	Leu	Tyr	Ile	Lys	Asp 185	Val	Gln	Asn	Glu	Asp 190	Gly	Leu
Tyr	Asn	Tyr 195	Arg	Cys	Ile	Thr	Arg 200	His	Arg	Tyr	Thr	Gly 205	Glu	Thr	Arg
Gln	Ser 210	Asn	Ser	Ala	Arg	Leu 215	Phe	Val	Ser	Asp	Pro 220	Ala	Asn	Ser	Ala
Pro 225	Ser	Ile	Leu	Asp	Gly 230	Phe	Asp	His	Arg	Lys 235	Ala	Met	Ala	Gly	Gln 240
Arg	Val	Glu	Leu	Pro 245	Cys	Lys	Ala	Leu	Gly 250	His	Pro	Glu	Pro	Asp 255	Tyr
Arg	Trp	Leu	Lys 260	Asp	Asn	Met	Pro	Leu 265	Glu	Leu	Ser	Gly	Arg 270	Phe	Gln

Lys Thr Val Thr Gly Leu Leu Ile Glu Asn Ile Arg Pro Ser Asp Ser
 275 280 285
 Gly Ser Tyr Val Cys Glu Val Ser Asn Arg Tyr Gly Thr Ala Lys Val
 290 295 300
 Ile Gly Arg Leu Tyr Val Lys Gln Pro Leu Lys Ala Thr Ile Ser Pro
 305 310 315 320
 Arg Lys Val Lys Ser Ser Val Gly Ser Gln Val Ser Leu Ser Cys Ser
 325 330 335
 Val Thr Gly Thr Glu Asp Gln Glu Leu Ser Trp Tyr Arg Asn Gly Glu
 340 345 350
 Ile Leu Asn Pro Gly Lys Asn Val Arg Ile Thr Gly Ile Asn His Glu
 355 360 365
 Asn Leu Ile Met Asp His Met Val Lys Ser Asp Gly Gly Ala Tyr Gln
 370 375 380
 Cys Phe Val Arg Lys Asp Lys Leu Ser Ala Gln Asp Tyr Val Gln Val
 385 390 395 400
 Val Leu Glu Asp Gly Thr Pro Lys Ile Ile Ser Ala Phe Ser Glu Lys
 405 410 415
 Val Val Ser Pro Ala Glu Pro Val Ser Leu Met Cys Asn Val Lys Gly
 420 425 430
 Thr Pro Leu Pro Thr Ile Thr Trp Thr Leu Asp Asp Asp Pro Ile Leu
 435 440 445
 Lys Gly Gly Ser His Arg Ile Ser Gln Met Ile Thr Ser Glu Gly Asn
 450 455 460
 Val Val Ser Tyr Leu Asn Ile Ser Ser Ser Gln Val Arg Asp Gly Gly
 465 470 475 480
 Val Tyr Arg Cys Thr Ala Asn Asn Ser Ala Gly Val Val Leu Tyr Gln
 485 490 495
 Ala Arg Ile Asn Val Arg Gly Pro Ala Ser Ile Arg Pro Met Lys Asn
 500 505 510
 Ile Thr Ala Ile Ala Gly Arg Asp Thr Tyr Ile His Cys Arg Val Ile
 515 520 525
 Gly Tyr Pro Tyr Tyr Ser Ile Lys Trp Tyr Lys Asn Ser Asn Leu Leu
 530 535 540
 Pro Phe Asn His Arg Gln Val Ala Phe Glu Asn Asn Gly Thr Leu Lys
 545 550 555 560
 Leu Ser Asp Val Gln Lys Glu Val Asp Glu Gly Glu Tyr Thr Cys Asn
 565 570 575
 Val Leu Val Gln Pro Gln Leu Ser Thr Ser Gln Ser Val His Val Thr
 580 585 590
 Val Lys Val Pro Pro Phe Ile Gln Pro Phe Glu Phe Pro Arg Phe Ser
 595 600 605

0055591 10397

Ile	Gly	Gln	Arg	Val	Phe	Ile	Pro	Cys	Val	Val	Ser	Gly	Asp	Leu	
610						615				620					
Pro	Ile	Thr	Ile	Thr	Trp	Gln	Lys	Asp	Gly	Arg	Pro	Ile	Pro	Gly	Ser
625					630					635					640
Leu	Gly	Val	Thr	Ile	Asp	Asn	Ile	Asp	Phe	Thr	Ser	Ser	Leu	Arg	Ile
				645					650					655	
Ser	Asn	Leu	Ser	Leu	Met	His	Asn	Gly	Asn	Tyr	Thr	Cys	Ile	Ala	Arg
			660					665					670		
Asn	Glu	Ala	Ala	Ala	Val	Glu	His	Gln	Ser	Gln	Leu	Ile	Val	Arg	Val
		675					680					685			
Pro	Pro	Lys	Phe	Val	Val	Gln	Pro	Arg	Asp	Gln	Asp	Gly	Ile	Tyr	Gly
	690					695				700					
Lys	Ala	Val	Ile	Leu	Asn	Cys	Ser	Ala	Glu	Gly	Tyr	Pro	Val	Pro	Thr
705					710					715					720
Ile	Val	Trp	Lys	Phe	Ser	Lys	Gly	Ala	Gly	Val	Pro	Gln	Phe	Gln	Pro
				725					730					735	
Ile	Ala	Leu	Asn	Gly	Arg	Ile	Gln	Val	Leu	Ser	Asn	Gly	Ser	Leu	Leu
			740					745					750		
Ile	Lys	His	Val	Val	Glu	Glu	Asp	Ser	Gly	Tyr	Tyr	Leu	Cys	Lys	Val
		755					760					765			
Ser	Asn	Asp	Val	Gly	Ala	Asp	Val	Ser	Lys	Ser	Met	Tyr	Leu	Thr	Val
						775					780				
Lys	Ile	Pro	Ala	Met	Ile	Thr	Ser	Tyr	Pro	Asn	Thr	Thr	Leu	Ala	Thr
785					790					795					800
Gln	Gly	Gln	Lys	Lys	Glu	Met	Ser	Cys	Thr	Ala	His	Gly	Glu	Lys	Pro
				805					810					815	
Ile	Ile	Val	Arg	Trp	Glu	Lys	Glu	Asp	Arg	Ile	Ile	Asn	Pro	Glu	Met
			820					825					830		
Ala	Arg	Tyr	Leu	Val	Ser	Thr	Lys	Glu	Val	Gly	Glu	Glu	Val	Ile	Ser
		835					840					845			
Thr	Leu	Gln	Ile	Leu	Pro	Thr	Val	Arg	Glu	Asp	Ser	Gly	Phe	Phe	Ser
	850					855					860				
Cys	His	Ala	Ile	Asn	Ser	Tyr	Gly	Glu	Asp	Arg	Gly	Ile	Ile	Gln	Leu
865				870						875					880
Thr	Val	Gln	Glu	Pro	Pro	Asp	Pro	Pro	Glu	Ile	Glu	Ile	Lys	Asp	Val
				885					890					895	
Lys	Ala	Arg	Thr	Ile	Thr	Leu	Arg	Trp	Thr	Met	Gly	Phe	Asp	Gly	Asn
			900					905					910		
Ser	Pro	Ile	Thr	Gly	Tyr	Asp	Ile	Glu	Cys	Lys	Asn	Lys	Ser	Asp	Ser
		915					920					925			
Trp	Asp	Ser	Ala	Gln	Arg	Thr	Lys	Asp	Val	Ser	Pro	Gln	Leu	Asn	Ser
930						935					940				

Ala Thr Ile Ile Asp Ile His Pro Ser Ser Thr Tyr Ser Ile Arg Met
 945 950 955 960
 Tyr Ala Lys Asn Arg Ile Gly Lys Ser Glu Pro Ser Asn Glu Leu Thr
 965 970 975
 Ile Thr Ala Asp Glu Ala Ala Pro Asp Gly Pro Pro Gln Glu Val His
 980 985 990
 Leu Glu Pro Ile Ser Ser Gln Ser Ile Arg Val Thr Trp Lys Ala Pro
 995 1000 1005
 Lys Lys His Leu Gln Asn Gly Ile Ile Arg Gly Tyr Gln Ile Gly Tyr
 1010 1015 1020
 Arg Glu Tyr Ser Thr Gly Gly Asn Phe Gln Phe Asn Ile Ile Ser Val
 1025 1030 1035 1040
 Asp Thr Ser Gly Asp Ser Glu Val Tyr Thr Leu Asp Asn Leu Asn Lys
 1045 1050 1055
 Phe Thr Gln Tyr Gly Leu Val Val Gln Ala Cys Asn Arg Ala Gly Thr
 1060 1065 1070
 Gly Pro Ser Ser Gln Glu Ile Ile Thr Thr Thr Leu Glu Asp Val Pro
 1075 1080 1085
 Ser Tyr Pro Pro Glu Asn Val Gln Ala Ile Ala Thr Ser Pro Glu Ser
 1090 1095 1100
 Ile Ser Ile Ser Trp Ser Thr Leu Ser Lys Glu Ala Leu Asn Gly Ile
 1105 1110 1115 1120
 Leu Gln Gly Phe Arg Val Ile Tyr Trp Ala Asn Leu Met Asp Gly Glu
 1125 1130 1135
 Leu Gly Glu Ile Lys Asn Ile Thr Thr Thr Gln Pro Ser Leu Glu Leu
 1140 1145 1150
 Asp Gly Leu Glu Lys Tyr Thr Asn Tyr Ser Ile Gln Val Leu Ala Phe
 1155 1160 1165
 Thr Arg Ala Gly Asp Gly Val Arg Ser Glu Gln Ile Phe Thr Arg Thr
 1170 1175 1180
 Lys Glu Asp Val Pro Gly Pro Pro Ala Gly Val Lys Ala Ala Ala Ala
 1185 1190 1195 1200
 Ser Ala Ser Met Val Phe Val Ser Trp Leu Pro Pro Leu Lys Leu Asn
 1205 1210 1215
 Gly Ile Ile Arg Lys Tyr Thr Val Phe Cys Ser His Pro Tyr Pro Thr
 1220 1225 1230
 Val Ile Ser Glu Phe Glu Ala Ser Pro Asp Ser Phe Ser Tyr Arg Ile
 1235 1240 1245
 Pro Asn Leu Ser Arg Asn Arg Gln Tyr Ser Val Trp Val Val Ala Val
 1250 1255 1260
 Thr Ser Ala Gly Arg Gly Asn Ser Ser Glu Ile Ile Thr Val Glu Pro
 1265 1270 1275 1280

00956994 1033 452201 15525580

Arg Arg Arg Arg Arg Glu Gln Arg Leu Lys Arg Leu Arg Asp Ala Lys
 1620 1625 1630
 Ser Leu Ala Glu Met Leu Met Ser Lys Asn Thr Arg Thr Ser Asp Thr
 1635 1640 1645
 Leu Ser Lys Gln Gln Gln Thr Leu Arg Met His Ile Asp Ile Pro Arg
 1650 1655 1660
 Ala Gln Leu Leu Ile Glu Glu Arg Asp Thr Met Glu Thr Ile Asp Asp
 1665 1670 1675 1680
 Arg Ser Thr Val Leu Leu Thr Asp Ala Asp Phe Gly Glu Ala Ala Lys
 1685 1690 1695
 Gln Lys Ser Leu Thr Val Thr His Thr Val His Tyr Gln Ser Val Ser
 1700 1705 1710
 Gln Ala Thr Gly Pro Leu Val Asp Val Ser Asp Ala Arg Pro Gly Thr
 1715 1720 1725
 Asn Pro Thr Thr Arg Arg Asn Ala Lys Ala Gly Pro Thr Ala Arg Asn
 1730 1735 1740
 Arg Tyr Ala Ser Gln Trp Thr Leu Asn Arg Pro His Pro Thr Ile Ser
 1745 1750 1755 1760
 Ala His Thr Leu Thr Thr Asp Trp Arg Leu Pro Thr Pro Arg Ala Ala
 1765 1770 1775
 Gly Ser Val Asp Lys Glu Ser Asp Ser Tyr Ser Val Ser Pro Ser Gln
 1780 1785 1790
 Asp Thr Asp Arg Ala Arg Ser Ser Met Val Ser Thr Glu Ser Ala Ser
 1795 1800 1805
 Ser Thr Tyr Glu Glu Leu Ala Arg Ala Tyr Glu His Ala Lys Met Glu
 1810 1815 1820
 Glu Gln Leu Arg His Ala Lys Phe Thr Ile Thr Glu Cys Phe Ile Ser
 1825 1830 1835 1840
 Asp Thr Ser Ser Glu Gln Leu Thr Ala Gly Thr Asn Glu Tyr Thr Asp
 1845 1850 1855
 Ser Leu Thr Ser Ser Thr Pro Ser Glu Ser Gly Ile Cys Arg Phe Thr
 1860 1865 1870
 Ala Ser Pro Pro Lys Pro Gln Asp Gly Gly Arg Val Met Asn Met Ala
 1875 1880 1885
 Val Pro Lys Ala Ile Gly Gln Val Thr Ser Tyr Ile Cys Leu His Thr
 1890 1895 1900
 Leu Glu Trp Thr Phe Cys
 1905 1910

036694 10229

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGGTATTC TTACTCATGA GCATTTTCAGC TAAACTCTTT GCATCTCGCA GCCTCTTTAG	60
CCTCTGCTCC CGCCGCCTCC TCCGCACAAC CAGCAGGAGC ACAAACAGCA GCAAGACCCC	120
CACCAGGATA CAGGAGATGG TCACCAGCAT CTGAGCCCC TCGTTGGTCG TCAGCCCTTC	180
TTCGTTTTGG ACAACTGACT TAATGAGTGG AGGAATTGTA CTGCCATCGT AGTTCAGCGT	240
AGCGAAGTTG GCCTGCTTCT CCGCGCAGCC CGCACTGTTG CACACCCGCA TCTGCAGCTC	300
ATACCAGGTG GCTTCCTGCA GGTACATACAG GATGTAGGAC TTGGAGAGAG AGGTCCTCTG	360
AGCTGTGGTC CAAACTGTGG TCCCAAAG	388

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTGATGCTC GAGTGAATTC	20
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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCAGTTCTCA AAGGAGCAGG	20
-----------------------	----

46307-169630

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGGGCCCGGG	CGCGGCGGAG	CGCAGCGCAA	CGCGGGGGGC	GAGGCCGGCG	CGTGGCTCGC	60
TCGCTGGCTC	GCTGGCTCGC	GGGAGGCCGG	GCAGCAGCAG	GGGCATGTGG	ATACTGGCTC	120
TCTCCTTGTT	CCAGAGCTTC	GCGAATGTTT	TCAGTGAAGA	GCCCCACTCC	AGCCTCTACT	180
TTGTCAATGC	ATCGCTGCAA	GAGGTAGTGT	TTGCAAGCAC	ATCGGGGACG	CTGGTGCCCT	240
GCCCGGCTGC	AGGCATCCCT	CCTGTGACTC	TCAGATGGTA	CCTAGCAACG	GGCGAGGAGA	300
TCTACGATGT	CCCCGGGATC	CGCCACGTCC	ATCCCAATGG	CACTCTCCAA	ATTTTCCCCT	360
TTCTCCTTC	AAGCTTCAGC	ACCTTAATCC	ATGATAATAC	TTACTATTGC	ACAGCTGAAA	420
ACCCTTCAGG	GAAAATTAGA	AGTCAGGATG	TCCACATCAA	GGCTGTTTTA	CGGGAGCCCT	480
ATACAGTCCG	TGTGGAGGAC	CAGAAAACCA	TGAGAGGCAA	TGTCGCGGTG	TTCAAGTGCA	540
TTATCCCCTC	CTCGGTGGAG	GCGTACGTCT	CTGTCTCTC	ATGGGAGAAA	GACACGGTTT	600
CACTTGTCTC	AGGATCTAGA	TTTCTCATCA	CATCCACGGG	AGCCTTGTAT	ATTAAAGATG	660
TTCAGAACGA	AGATGGGCTG	TACAACTACC	GCTGCATCGC	GCGGCACAGA	TTCGCGGGGG	720
AGACGAGACA	GAGCAACTGC	GCGAGACTGT	TCGTGTCAGA	ACCAGCAAAC	TCAGCCCATC	780
CATCCTGGAA	GGGTTTGACC	ACCGCCAAAC	CATGGCCGGG	CACGCGTGGA	GCTGCCTTGC	840
CA						842

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 898 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGCCGGCCGG	TTGCAAGCCT	GTACTACAGG	CCATACTGCG	TGAATTATCA	GGTTGTCCAG	60
GGTGTACACT	TCGCTGTCCC	GGTGGTGTCA	ATACTGATGA	TGTTGAACTG	GAAGTTACCC	120
CGTGCTGTAC	TCCGGTAGCC	TATTGGTAGC	CGCGAATGAT	CCCGTCTTGT	ATAGTGTCTT	180
TGGGAGCCTC	TCCAGGTAAC	CCTGATACTC	TGAGATGAGG	TGGGTTCCAA	GTGAACTTCC	240
TGAGGTGGAC	ATCACGAGCT	GCCTCATCCG	CCGTGATGGT	GATCTCGTTG	CTGGGCTCAC	300
TCTTGCCAAT	CCGGTTCTTG	GCGTACATGC	GGATGCTGTA	GGTGGAGGAA	GGGTGGATAT	360
CAATGATGGT	GGCCGAGTTC	AGCTGAGGGG	AAACATCTTT	GGTTCTCTGA	GCAGAATCCC	420
ACGAGTCTGA	TTTATTTTTG	CATTCACT	GTCATAGCCT	GTGATGGGGC	TGTTGCCATC	480
AAACCCCATG	GTCCACCTGA	GCGTGATGGT	GCGAGCTTTG	ACATCTCTTG	ATCTCAATCT	540
CGGGAGGATC	TGGGGGTTCT	TGCACTGTGA	GTTGAATTAT	TCCACGGTCC	TCCCCGTATG	600
AATTGATAGC	ATGGCAGGAG	AAGAAACCGG	AATCTTCTCT	CACTGTTGGC	AAAATCTGCA	660
GCGTAGATAT	CACTTCCTCT	CCCACCTCCT	TGGTGGATAC	AGTACGGGCC	ACTTTCAGGG	720
TTAATGATCC	TGTCTCTCTT	CTCCAGCGGA	CAATGATGGG	CTCTCCCATG	GGCTGTGCAG	780
CTCATTCCTT	CCTTTGACCC	TGATGGCCAG	GTGGTGTGGG	TATAAGTTAT	ATCATGGCCC	840
GAATTTCCCT	GTGAGTCCAT	GGAATTGCTG	AACGTTCTGC	GCCCACATCG	TTGCTGA	898

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCACCATTC	ACACACCCAG	ACATGGCGGG	TTGCGGCAA	CCTTCAGTTC	CTGGCCTTCC	60
TGTAGGGTAA	AGGGCTGCTG	CGGGTTTATA	GACCGGCACA	TGCCCATCCT	GGCATACGGT	120
GGCCAGTGGC	TTTCCATCTG	GATTCCAGGC	CAAGCTAAAA	ATCTGTTTCT	GATGGCCCTG	180

ACAATTAACG AGCCAATCAA GCTACTTTTT TATGAATTCC GATATTTATA ATTAAGAATT 2160
GCCAAATATA TTA 2173

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 453..5168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGACTGAGGC CGGAGCACGG CAAAGATGAG CCTGCCCCGCC CGCCTGCTGC CTGGATGCGG	60
AGGGTGAGGG CTGGCGCACG GGAGGCCGCT GGCTGCGCAT TCTGGGCGCC GAGTGCCCGG	120
GATGAGCTCA CGCCCGCGTC TCGGCTCTC TCCACCTGCC GACCTGCCGG GGGCCCACTG	180
AGCTGACGGC GCACCTGGGC TCCGGCCGCA GCGTGGGGCG CGGCGCCCGG GAGCAGGTGT	240
GCAGGAGCGC AGCGCGCGGC GAGCGCAGCC CTCGCTCCGG AGCCCGGCCG CGCCGCGTGC	300
CCGGGCGGCT AGGCAGCGGC GCGGCGGGCG GCGGGCGGGC GGCGGGCGGC GGCCCCCGGG	360
CAGGTGCCGA GCGGCGAGCG GAGCCGGGCC GGGCGGAGCG CGGGGGGCGA GGCCGGCGCG	420
TCGCTCGCGG GAGGCCGGGG AGCGGCAGGG GC ATG TGG ATA CTG GCT CTC TCC	473
Met Trp Ile Leu Ala Leu Ser	
1 5	
TTG TTC CAG AGC TTC GCG AAT GTT TTC AGT GAA GAC CTA CAC TCC AGC	521
Leu Phe Gln Ser Phe Ala Asn Val Phe Ser Glu Asp Leu His Ser Ser	
10 15 20	
CTC TAC TTT GTC AAT GCA TCT CTG CAA GAG GTA GTG TTT GCC AGC ACC	569
Leu Tyr Phe Val Asn Ala Ser Leu Gln Glu Val Val Phe Ala Ser Thr	
25 30 35	
ACG GGG ACT CTG GTG CCC TGC CCC GCA GCA GGC ATC CCT CCT GTG ACT	617
Thr Gly Thr Leu Val Pro Cys Pro Ala Ala Gly Ile Pro Pro Val Thr	
40 45 50 55	
CTC AGA TGG TAC CTA GCC ACG GGC GAG GAG ATC TAC GAT GTC CCC GGG	665
Leu Arg Trp Tyr Leu Ala Thr Gly Glu Glu Ile Tyr Asp Val Pro Gly	
60 65 70	
ATC CGC CAC GTC CAC CCC AAC GGC ACT CTC CAA ATT TTC CCC TTC CCT	713
Ile Arg His Val His Pro Asn Gly Thr Leu Gln Ile Phe Pro Phe Pro	
75 80 85	
CCT TCA AGC TTC AGT ACC TTA ATC CAT GAT AAT ACT TAT TAT TGC ACA	761
Pro Ser Ser Phe Ser Thr Leu Ile His Asp Asn Thr Tyr Tyr Cys Thr	
90 95 100	

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GCT	GAA	AAT	CCT	TCA	GGG	AAA	ATT	AGA	AGT	CAG	GAT	GTC	CAC	ATC	AAG	809
Ala	Glu	Asn	Pro	Ser	Gly	Lys	Ile	Arg	Ser	Gln	Asp	Val	His	Ile	Lys	
105						110					115					
GCT	GTT	TTA	CGG	GAG	CCC	TAT	ACA	GTC	CGT	GTG	GAG	GAC	CAG	AAA	ACC	857
Ala	Val	Leu	Arg	Glu	Pro	Tyr	Thr	Val	Arg	Val	Glu	Asp	Gln	Lys	Thr	
120					125					130					135	
ATG	AGA	GGC	AAT	GTT	GCG	GTC	TTC	AAG	TGC	ATT	ATC	CCC	TCC	TCG	GTG	905
Met	Arg	Gly	Asn	Val	Ala	Val	Phe	Lys	Cys	Ile	Ile	Pro	Ser	Ser	Val	
				140					145					150		
GAG	GCG	TAC	ATC	ACT	GTC	GTC	TCA	TGG	GAG	AAA	GAC	ACT	GTT	TCA	CTT	953
Glu	Ala	Tyr	Ile	Thr	Val	Val	Ser	Trp	Glu	Lys	Asp	Thr	Val	Ser	Leu	
			155					160					165			
GTC	TCA	GGA	TCT	AGA	TTT	CTC	ATC	ACA	TCC	ACG	GGA	GCC	TTG	TAT	ATT	1001
Val	Ser	Gly	Ser	Arg	Phe	Leu	Ile	Thr	Ser	Thr	Gly	Ala	Leu	Tyr	Ile	
		170					175					180				
AAA	GAT	GTA	CAG	AAT	GAA	GAT	GGA	TTG	TAT	AAC	TAC	CGC	TGC	ATC	ACG	1049
Lys	Asp	Val	Gln	Asn	Glu	Asp	Gly	Leu	Tyr	Asn	Tyr	Arg	Cys	Ile	Thr	
185						190					195					
CGG	CAT	CGA	TAC	ACC	GGA	GAG	ACG	AGG	CAG	AGC	AAC	AGC	GCC	AGA	CTT	1097
Arg	His	Arg	Tyr	Thr	Gly	Glu	Thr	Arg	Gln	Ser	Asn	Ser	Ala	Arg	Leu	
200					205					210					215	
TTT	GTA	TCA	GAC	CCA	GCG	AAC	TCA	GCC	CCA	TCC	ATA	CTG	GAT	GGG	TTT	1145
Phe	Val	Ser	Asp	Pro	Ala	Asn	Ser	Ala	Pro	Ser	Ile	Leu	Asp	Gly	Phe	
				220					225					230		
GAC	CAT	CGC	AAA	GCC	ATG	GCT	GGG	CAG	CGT	GTG	GAG	CTG	CCT	TGC	AAA	1193
Asp	His	Arg	Lys	Ala	Met	Ala	Gly	Gln	Arg	Val	Glu	Leu	Pro	Cys	Lys	
			235					240					245			
GCG	CTC	GGG	CAC	CCT	GAG	CCA	GAT	TAC	CGC	TGG	CTG	AAG	GAC	AAC	ATG	1241
Ala	Leu	Gly	His	Pro	Glu	Pro	Asp	Tyr	Arg	Trp	Leu	Lys	Asp	Asn	Met	
		250					255					260				
CCC	CTG	GAA	CTT	TCA	GGG	AGG	TTC	CAG	AAG	ACC	GTG	ACG	GGG	CTG	CTC	1289
Pro	Leu	Glu	Leu	Ser	Gly	Arg	Phe	Gln	Lys	Thr	Val	Thr	Gly	Leu	Leu	
		265				270					275					
ATT	GAG	AAC	ATT	CGC	CCC	TCG	GAC	TCA	GGC	AGC	TAT	GTT	TGT	GAA	GTG	1337
Ile	Glu	Asn	Ile	Arg	Pro	Ser	Asp	Ser	Gly	Ser	Tyr	Val	Cys	Glu	Val	
280					285					290					295	
TCC	AAC	AGA	TAC	GGA	ACT	GCT	AAG	GTG	ATA	GGC	CGC	CTG	TAC	GTG	AAA	1385
Ser	Asn	Arg	Tyr	Gly	Thr	Ala	Lys	Val	Ile	Gly	Arg	Leu	Tyr	Val	Lys	
				300					305					310		
CAG	CCA	CTG	AAA	GCC	ACC	ATC	AGT	CCC	AGG	AAG	GTT	AAA	AGC	AGC	GTG	1433
Gln	Pro	Leu	Lys	Ala	Thr	Ile	Ser	Pro	Arg	Lys	Val	Lys	Ser	Ser	Val	
			315					320					325			
GGT	AGC	CAA	GTT	TCC	TTG	TCC	TGC	AGC	GTG	ACA	GGA	ACT	GAG	GAC	CAG	1481
Gly	Ser	Gln	Val	Ser	Leu	Ser	Cys	Ser	Val	Thr	Gly	Thr	Glu	Asp	Gln	
		330					335					340				
GAA	CTC	TCC	TGG	TAC	CGC	AAT	GGT	GAA	ATC	CTC	AAC	CCT	GGA	AAA	AAT	1529
Glu	Leu	Ser	Trp	Tyr	Arg	Asn	Gly	Glu	Ile	Leu	Asn	Pro	Gly	Lys	Asn	
		345				350					355					

GTG Val 360	AGG Arg	ATC Ile	ACA Thr	GGG Gly 365	ATC Ile 365	AAC Asn	CAC His	GAA Glu	AAC Asn	CTT Leu 370	ATA Ile	ATG Met	GAT Asp	CAC His	ATG Met 375	1577
GTC Val	AAA Lys	AGT Ser	GAC Asp	GGG Gly 380	GGC Gly	GCA Ala	TAC Tyr	CAG Gln	TGC Cys 385	TTT Phe	GTG Val	CGC Arg	AAG Lys	GAC Asp 390	AAG Lys	1625
CTG Leu	TCC Ser	GCT Ala	CAA Gln 395	GAC Asp	TAT Tyr	GTG Val	CAG Gln	GTG Val 400	GTC Val	CTT Leu	GAA Glu	GAT Asp	GGA Gly 405	ACT Thr	CCC Pro	1673
AAA Lys	ATT Ile 410	ATT Ile	TCT Ser	GCC Ala	TTT Phe	AGT Ser	GAA Glu 415	AAG Lys	GTG Val	GTG Val	AGT Ser	CCA Pro 420	GCA Ala	GAG Glu	CCG Pro	1721
GTT Val	TCC Ser 425	CTT Leu	ATG Met	TGC Cys	AAC Asn 430	GTG Val	AAG Lys	GGA Gly	ACA Thr	CCT Pro 435	TTG Leu	CCC Pro	ACG Thr	ATC Ile	ACG Thr	1769
TGG Trp 440	ACC Thr	CTG Leu	GAC Asp	GAT Asp 445	GAC Asp 445	CCG Pro	ATT Ile	CTC Leu	AAG Lys	GGT Gly 450	GGC Gly	AGT Ser	CAC His	CGC Arg	ATC Ile 455	1817
AGC Ser	CAG Gln	ATG Met	ATC Ile 460	ACG Thr 460	TCG Ser	GAG Glu	GGG Gly	AAC Asn 465	GTG Val 465	GTC Val	AGC Ser	TAC Tyr	CTG Leu	AAC Asn 470	ATC Ile	1865
TCC Ser	AGC Ser	TCC Ser	CAG Gln 475	GTC Val	CGG Arg	GAC Asp	GGG Gly 480	GGA Gly 480	GTC Val	TAC Tyr	CGC Arg	TGC Cys	ACT Thr 485	GCC Ala	AAC Asn	1913
AAC Asn	TCG Ser 490	GCG Ala	GGA Gly 490	GTC Val	GTC Val	CTG Leu 495	TAC Tyr 495	CAG Gln	GCT Ala	CGA Arg	ATA Ile	AAC Asn 500	GTA Val	AGA Arg	GGG Gly	1961
CCT Pro 505	GCA Ala	AGC Ser	ATT Ile	CGA Arg	CCA Pro	ATG Met 510	AAA Lys	AAC Asn	ATC Ile	ACA Thr 515	GCA Ala	ATA Ile	GCA Ala	GGA Gly	CGG Arg	2009
GAC Asp 520	ACA Thr	TAC Tyr	ATT Ile	CAC His 525	TGT Cys	CGT Arg	GTG Val	ATT Ile	GGC Gly	TAT Tyr 530	CCG Pro	TAT Tyr	TAC Tyr	TCC Ser	ATT Ile 535	2057
AAA Lys	TGG Trp	TAC Tyr	AAG Lys	AAC Asn 540	TCT Ser	AAC Asn	CTG Leu	CTT Leu	CCT Pro 545	TTC Phe	AAC Asn	CAC His	CGC Arg	CAA Gln 550	GTG Val	2105
GCA Ala	TTT Phe	GAG Glu	AAC Asn 555	AAT Asn	GGA Gly	ACT Thr	CTT Leu	AAA Lys 560	CTT Leu	TCA Ser	GAT Asp	GTG Val	CAA Gln 565	AAG Lys	GAA Glu	2153
GTG Val	GAC Asp 570	GAG Glu	GGG Gly	GAG Glu	TAC Tyr	ACG Thr	TGC Cys 575	AAC Asn	GTG Val	TTG Leu	GTT Val	CAA Gln 580	CCA Pro	CAA Gln	CTC Leu	2201
TCC Ser 585	ACC Thr	AGC Ser	CAG Gln	AGC Ser	GTC Val	CAC His 590	GTG Val	ACC Thr	GTG Val	AAA Lys 595	GTT Val	CCG Pro	CCT Pro	TTC Phe	ATA Ile	2249
CAA Gln 600	CCC Pro	TTT Phe	GAG Glu	TTT Phe	CCA Pro 605	AGA Arg	TTC Phe	TCC Ser	ATT Ile	GGG Gly 610	CAG Gln	CGG Arg	GTC Val	TTC Phe	ATC Ile 615	2297

CCC Pro	TGT Cys	GTT Val	GTG Val	GTC Val 620	TCA Ser	GGG Gly	GAC Asp	TTA Leu	CCC Pro 625	ATC Ile	ACG Thr	ATC Ile	ACC Thr	TGG Trp 630	CAG Gln	2345
AAG Lys	GAT Asp	GGC Gly	CGG Arg 635	CCA Pro	ATC Ile	CCT Pro	GGG Gly	AGC Ser 640	CTT Leu	GGG Gly	GTG Val	ACC Thr	ATT Ile 645	GAC Asp	AAT Asn	2393
ATT Ile	GAC Asp	TTC Phe 650	ACG Thr	AGC Ser	TCC Ser	TTG Leu	AGG Arg 655	ATT Ile	TCC Ser	AAT Asn	CTC Leu	TCG Ser 660	CTC Leu	ATG Met	CAC His	2441
AAT Asn	GGG Gly 665	AAT Asn	TAC Tyr	ACC Thr	TGC Cys	ATA Ile 670	GCC Ala	CGG Arg	AAT Asn	GAG Glu	GCC Ala 675	GCC Ala	GCT Ala	GTG Val	GAG Glu	2489
CAC His 680	CAA Gln	AGC Ser	CAG Gln	TTG Leu	ATT Ile 685	GTC Val	AGA Arg	GTT Val	CCT Pro	CCC Pro 690	AAG Lys	TTT Phe	GTG Val	GTT Val	CAG Gln 695	2537
CCA Pro	CGG Arg	GAC Asp	CAG Gln 700	GAC Asp	GGG Gly	ATT Ile	TAT Tyr	GGC Gly	AAA Lys 705	GCA Ala	GTC Val	ATC Ile	CTC Leu	AAT Asn 710	TGT Cys	2585
TCT Ser	GCT Ala	GAG Glu	GGT Gly 715	TAC Tyr	CCT Pro	GTA Val	CCT Pro	ACC Thr 720	ATC Ile	GTG Val	TGG Trp	AAA Lys	TTC Phe 725	TCT Ser	AAA Lys	2633
GGT Gly	GCT Ala	GGG Gly 730	GTT Val	CCC Pro	CAG Gln	TTC Phe	CAG Gln 735	CCA Pro	ATT Ile	GCC Ala	CTA Leu	AAT Asn 740	GGC Gly	CGA Arg	ATC Ile	2681
CAA Gln	GTT Val 745	CTC Leu	AGC Ser	AAT Asn	GGG Gly	TCG Ser 750	TTG Leu	CTG Leu	ATC Ile	AAG Lys	CAT His 755	GTC Val	GTG Val	GAG Glu	GAA Glu	2729
GAC Asp 760	AGT Ser	GGC Gly	TAC Tyr	TAC Tyr	CTC Leu 765	TGC Cys	AAG Lys	GTC Val	AGC Ser	AAC Asn 770	GAT Asp	GTG Val	GGC Gly	GCA Ala	GAC Asp 775	2777
GTC Val	AGC Ser	AAG Lys	TCC Ser	ATG Met 780	TAC Tyr	CTC Leu	ACG Thr	GTT Val	AAA Lys 785	ATT Ile	CCT Pro	GCG Ala	ATG Met	ATA Ile 790	ACA Thr	2825
TCC Ser	TAT Tyr	CCA Pro	AAT Asn 795	ACT Thr	ACC Thr	CTG Leu	GCC Ala	ACG Thr 800	CAG Gln	GGG Gly	CAG Gln	AAA Lys	AAG Lys 805	GAG Glu	ATG Met	2873
AGC Ser	TGC Cys	ACG Thr 810	GCG Ala	CAT His	GGT Gly	GAG Glu	AAG Lys 815	CCC Pro	ATT Ile	ATA Ile	GTC Val	CGC Arg 820	TGG Trp	GAG Glu	AAG Lys	2921
GAG Glu	GAC Asp 825	CGA Arg	ATC Ile	ATT Ile	AAC Asn	CCT Pro 830	GAG Glu	ATG Met	GCC Ala	CGT Arg	TAT Tyr 835	CTT Leu	GTG Val	TCC Ser	ACC Thr	2969
AAG Lys 840	GAG Glu	GTG Val	GGA Gly	GAA Glu	GAG Glu 845	GTG Val	ATT Ile	TCT Ser	ACT Thr	CTG Leu 850	CAG Gln	ATT Ile	TTG Leu	CCA Pro	ACT Thr 855	3017
GTG Val	AGA Arg	GAA Glu	GAT Asp	TCT Ser 860	GGT Gly	TTC Phe	TTT Phe	TCC Ser	TGC Cys 865	CAT His	GCT Ala	ATT Ile	AAT Asn	TCT Ser 870	TAT Tyr	3065

GGG GAG GAC CGT GGA ATA ATT CAG CTC ACA GTG CAA GAG CCC CCA GAC	3113
Gly Glu Asp Arg Gly Ile Ile Gln Leu Thr Val Gln Glu Pro Pro Asp	
875 880 885	
CCT CCC GAA ATT GAG ATC AAA GAT GTC AAA GCA CGC ACA ATT ACG CTC	3161
Pro Pro Glu Ile Glu Ile Lys Asp Val Lys Ala Arg Thr Ile Thr Leu	
890 895 900	
AGG TGG ACC ATG GGG TTT GAT GGA AAC AGT CCC ATC ACA GGC TAC GAT	3209
Arg Trp Thr Met Gly Phe Asp Gly Asn Ser Pro Ile Thr Gly Tyr Asp	
905 910 915	
ATT GAA TGC AAA AAT AAA TCA GAC TCC TGG GAT TCT GCT CAG AGA ACC	3257
Ile Glu Cys Lys Asn Lys Ser Asp Ser Trp Asp Ser Ala Gln Arg Thr	
920 925 930 935	
AAA GAT GTT TCC CCT CAG CTG AAC TCG GCC ACC ATC ATT GAT ATC CAC	3305
Lys Asp Val Ser Pro Gln Leu Asn Ser Ala Thr Ile Ile Asp Ile His	
940 945 950	
CCT TCC TCC ACC TAC AGC ATC CGC ATG TAC GCC AAG AAC CGG ATT GGC	3353
Pro Ser Ser Thr Tyr Ser Ile Arg Met Tyr Ala Lys Asn Arg Ile Gly	
955 960 965	
AAG AGC GAG CCC AGC AAC GAG CTC ACC ATC ACG GCG GAC GAG GCA GCT	3401
Lys Ser Glu Pro Ser Asn Glu Leu Thr Ile Thr Ala Asp Glu Ala Ala	
970 975 980	
CCT GAT GGT CCA CCT CAG GAA GTT CAC CTG GAG CCT ATA TCA TCT CAG	3449
Pro Asp Gly Pro Pro Gln Glu Val His Leu Glu Pro Ile Ser Ser Gln	
985 990 995	
AGC ATC AGG GTC ACA TGG AAG GCT CCC AAG AAA CAT TTG CAA AAT GGG	3497
Ser Ile Arg Val Thr Trp Lys Ala Pro Lys Lys His Leu Gln Asn Gly	
1000 1005 1010 1015	
ATT ATC CGT GGC TAC CAA ATA GGT TAC CGA GAG TAC AGC ACT GGG GGT	3545
Ile Ile Arg Gly Tyr Gln Ile Gly Tyr Arg Glu Tyr Ser Thr Gly Gly	
1020 1025 1030	
AAC TTC CAA TTC AAC ATT ATC AGT GTC GAC ACC AGC GGG GAC AGT GAG	3593
Asn Phe Gln Phe Asn Ile Ile Ser Val Asp Thr Ser Gly Asp Ser Glu	
1035 1040 1045	
GTT TAC ACC CTG GAC AAC CTG AAT AAG TTC ACT CAG TAC GGC CTG GTG	3641
Val Tyr Thr Leu Asp Asn Leu Asn Lys Phe Thr Gln Tyr Gly Leu Val	
1050 1055 1060	
GTG CAG GCC TGT AAC CGG GCC GGC ACG GGG CCT TCT TCT CAG GAA ATC	3689
Val Gln Ala Cys Asn Arg Ala Gly Thr Gly Pro Ser Ser Gln Glu Ile	
1065 1070 1075	
ATC ACC ACC ACT CTC GAG GAT GTG CCC AGT TAC CCC CCC GAA AAT GTC	3737
Ile Thr Thr Thr Leu Glu Asp Val Pro Ser Tyr Pro Pro Glu Asn Val	
1080 1085 1090 1095	
CAA GCC ATA GCA ACA TCA CCA GAA AGC ATA TCA ATA TCC TGG TCC ACA	3785
Gln Ala Ile Ala Thr Ser Pro Glu Ser Ile Ser Ile Ser Trp Ser Thr	
1100 1105 1110	
CTT TCC AAG GAA GCC TTG AAT GGA ATT CTC CAG GGG TTC AGA GTC ATT	3833
Leu Ser Lys Glu Ala Leu Asn Gly Ile Leu Gln Gly Phe Arg Val Ile	
1115 1120 1125	

TAC TGG GCC AAC CTC ATG GAC GGA GAG CTG GGT GAG ATT AAA AAC ATC Tyr Trp Ala Asn Leu Met Asp Gly Glu Leu Gly Glu Ile Lys Asn Ile 1130 1135 1140	3881
ACC ACC ACA CAG CCT TCA CTG GAG CTG GAC GGG CTG GAA AAG TAC ACC Thr Thr Thr Gln Pro Ser Leu Glu Leu Asp Gly Glu Lys Tyr Thr 1145 1150 1155	3929
AAC TAC AGC ATC CAG GTG CTG GCC TTC ACC CGC GCA GGA GAC GGG GTC Asn Tyr Ser Ile Gln Val Leu Ala Phe Thr Arg Ala Gly Asp Gly Val 1160 1165 1170 1175	3977
AGG AGT GAG CAG ATC TTC ACC CGG ACC AAA GAG GAT GTT CCA GGT CCT Arg Ser Glu Gln Ile Phe Thr Arg Thr Lys Glu Asp Val Pro Gly Pro 1180 1185 1190	4025
CCC GCG GGT GTG AAG GCA GCG GCG GCC TCA GCC TCC ATG GTC TTT GTG Pro Ala Gly Val Lys Ala Ala Ala Ser Ala Ser Met Val Phe Val 1195 1200 1205	4073
TCC TGG CTT CCC CCT CTC AAG CTG AAC GGC ATC ATC CGA AAG TAC ACT Ser Trp Leu Pro Pro Leu Lys Leu Asn Gly Ile Ile Arg Lys Tyr Thr 1210 1215 1220	4121
GTA TTC TGC TCC CAC CCC TAT CCC ACA GTG ATC AGC GAG TTT GAG GCC Val Phe Cys Ser His Pro Tyr Pro Thr Val Ile Ser Glu Phe Glu Ala 1225 1230 1235	4169
TCT CCC GAC TCG TTT TCC TAC AGA ATT CCC AAC CTG AGT AGG AAT CGT Ser Pro Asp Ser Phe Ser Tyr Arg Ile Pro Asn Leu Ser Arg Asn Arg 1240 1245 1250 1255	4217
CAG TAC AGC GTC TGG GTG GTG GCT GTT ACT TCA GCC GGA AGA GGC AAC Gln Tyr Ser Val Trp Val Val Ala Val Thr Ser Ala Gly Arg Gly Asn 1260 1265 1270	4265
AGC AGT GAA ATC ATC ACA GTC GAG CCA CTA GCA AAA GCT CCT GCA CGA Ser Ser Glu Ile Ile Thr Val Glu Pro Leu Ala Lys Ala Pro Ala Arg 1275 1280 1285	4313
ATC CTG ACC TTC AGT GGG ACA GTG ACT ACT CCA TGG ATG AAA GAC ATT Ile Leu Thr Phe Ser Gly Thr Val Thr Thr Pro Trp Met Lys Asp Ile 1290 1295 1300	4361
GTC TTG CCT TGT AAG GCT GTT GGG GAC CCT TCT CCT GCA GTC AAA TGG Val Leu Pro Cys Lys Ala Val Gly Asp Pro Ser Pro Ala Val Lys Trp 1305 1310 1315	4409
ATG AAA GAC AGT AAC GGG ACA CCC AGT CTA GTA ACG ATT GAT GGG CGG Met Lys Asp Ser Asn Gly Thr Pro Ser Leu Val Thr Ile Asp Gly Arg 1320 1325 1330 1335	4457
AGG AGC ATC TTT AGC AAC GGA AGC TTC ATT ATT CGC ACG GTG AAA GCA Arg Ser Ile Phe Ser Asn Gly Ser Phe Ile Ile Arg Thr Val Lys Ala 1340 1345 1350	4505
GAA GAC TCC GGC TAT TAC AGC TGC ATT GCC AAT AAC AAC TGG GGA TCT Glu Asp Ser Gly Tyr Tyr Ser Cys Ile Ala Asn Asn Asn Trp Gly Ser 1355 1360 1365	4553
GAT GAA ATT ATT TTA AAC TTA CAA GTA CAA GTT CCA CCA GAT CAG CCT Asp Glu Ile Ile Leu Asn Leu Gln Val Gln Val Pro Pro Asp Gln Pro 1370 1375 1380	4601

(2) INFORMATION FOR SEQ ID NO:11:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1571 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met 1	Trp	Ile	Leu	Ala 5	Leu	Ser	Leu	Phe	Gln 10	Ser	Phe	Ala	Asn	Val 15	Phe
Ser	Glu	Asp	Leu 20	His	Ser	Ser	Leu	Tyr 25	Phe	Val	Asn	Ala	Ser 30	Leu	Gln
Glu	Val	Val 35	Phe	Ala	Ser	Thr	Thr 40	Gly	Thr	Leu	Val	Pro 45	Cys	Pro	Ala
Ala	Gly 50	Ile	Pro	Pro	Val	Thr 55	Leu	Arg	Trp	Tyr	Leu 60	Ala	Thr	Gly	Glu
Glu 65	Ile	Tyr	Asp	Val	Pro 70	Gly	Ile	Arg	His	Val 75	His	Pro	Asn	Gly	Thr 80
Leu	Gln	Ile	Phe	Pro 85	Phe	Pro	Pro	Ser	Ser 90	Phe	Ser	Thr	Leu	Ile 95	His
Asp	Asn	Thr	Tyr 100	Tyr	Cys	Thr	Ala	Glu 105	Asn	Pro	Ser	Gly	Lys 110	Ile	Arg
Ser	Gln	Asp 115	Val	His	Ile	Lys	Ala 120	Val	Leu	Arg	Glu	Pro 125	Tyr	Thr	Val

Arg Val Glu Asp Gln Lys Thr Met Arg Gly Asn Val Ala Val Phe Lys
 130 135 140
 Cys Ile Ile Pro Ser Ser Val Glu Ala Tyr Ile Thr Val Val Ser Trp
 145 150 155 160
 Glu Lys Asp Thr Val Ser Leu Val Ser Gly Ser Arg Phe Leu Ile Thr
 165 170 175
 Ser Thr Gly Ala Leu Tyr Ile Lys Asp Val Gln Asn Glu Asp Gly Leu
 180 185 190
 Tyr Asn Tyr Arg Cys Ile Thr Arg His Arg Tyr Thr Gly Glu Thr Arg
 195 200 205
 Gln Ser Asn Ser Ala Arg Leu Phe Val Ser Asp Pro Ala Asn Ser Ala
 210 215 220
 Pro Ser Ile Leu Asp Gly Phe Asp His Arg Lys Ala Met Ala Gly Gln
 225 230 235 240
 Arg Val Glu Leu Pro Cys Lys Ala Leu Gly His Pro Glu Pro Asp Tyr
 245 250 255
 Arg Trp Leu Lys Asp Asn Met Pro Leu Glu Leu Ser Gly Arg Phe Gln
 260 265 270
 Lys Thr Val Thr Gly Leu Leu Ile Glu Asn Ile Arg Pro Ser Asp Ser
 275 280 285
 Gly Ser Tyr Val Cys Glu Val Ser Asn Arg Tyr Gly Thr Ala Lys Val
 290 295 300
 Ile Gly Arg Leu Tyr Val Lys Gln Pro Leu Lys Ala Thr Ile Ser Pro
 305 310 315 320
 Arg Lys Val Lys Ser Ser Val Gly Ser Gln Val Ser Leu Ser Cys Ser
 325 330 335
 Val Thr Gly Thr Glu Asp Gln Glu Leu Ser Trp Tyr Arg Asn Gly Glu
 340 345 350
 Ile Leu Asn Pro Gly Lys Asn Val Arg Ile Thr Gly Ile Asn His Glu
 355 360 365
 Asn Leu Ile Met Asp His Met Val Lys Ser Asp Gly Gly Ala Tyr Gln
 370 375 380
 Cys Phe Val Arg Lys Asp Lys Leu Ser Ala Gln Asp Tyr Val Gln Val
 385 390 395 400
 Val Leu Glu Asp Gly Thr Pro Lys Ile Ile Ser Ala Phe Ser Glu Lys
 405 410 415
 Val Val Ser Pro Ala Glu Pro Val Ser Leu Met Cys Asn Val Lys Gly
 420 425 430
 Thr Pro Leu Pro Thr Ile Thr Trp Thr Leu Asp Asp Asp Pro Ile Leu
 435 440 445
 Lys Gly Gly Ser His Arg Ile Ser Gln Met Ile Thr Ser Glu Gly Asn
 450 455 460

00556991 100397

Val 465	Val	Ser	Tyr	Leu	Asn 470	Ile	Ser	Ser	Ser	Gln 475	Val	Arg	Asp	Gly 480	
Val	Tyr	Arg	Cys	Thr 485	Ala	Asn	Asn	Ser	Ala 490	Gly	Val	Val	Leu	Tyr 495	Gln
Ala	Arg	Ile	Asn 500	Val	Arg	Gly	Pro	Ala 505	Ser	Ile	Arg	Pro	Met 510	Lys	Asn
Ile	Thr	Ala 515	Ile	Ala	Gly	Arg	Asp 520	Thr	Tyr	Ile	His	Cys 525	Arg	Val	Ile
Gly	Tyr 530	Pro	Tyr	Tyr	Ser	Ile 535	Lys	Trp	Tyr	Lys	Asn 540	Ser	Asn	Leu	Leu
Pro 545	Phe	Asn	His	Arg	Gln 550	Val	Ala	Phe	Glu	Asn 555	Asn	Gly	Thr	Leu	Lys 560
Leu	Ser	Asp	Val	Gln 565	Lys	Glu	Val	Asp	Glu 570	Gly	Glu	Tyr	Thr	Cys 575	Asn
Val	Leu	Val	Gln 580	Pro	Gln	Leu	Ser	Thr 585	Ser	Gln	Ser	Val	His 590	Val	Thr
Val	Lys	Val 595	Pro	Pro	Phe	Ile	Gln 600	Pro	Phe	Glu	Phe	Pro 605	Arg	Phe	Ser
Ile	Gly 610	Gln	Arg	Val	Phe	Ile 615	Pro	Cys	Val	Val	Val 620	Ser	Gly	Asp	Leu
Pro 625	Ile	Thr	Ile	Thr	Trp 630	Gln	Lys	Asp	Gly	Arg 635	Pro	Ile	Pro	Gly	Ser 640
Leu	Gly	Val	Thr	Ile 645	Asp	Asn	Ile	Asp	Phe 650	Thr	Ser	Ser	Leu	Arg 655	Ile
Ser	Asn	Leu	Ser 660	Leu	Met	His	Asn	Gly 665	Asn	Tyr	Thr	Cys	Ile 670	Ala	Arg
Asn	Glu	Ala 675	Ala	Ala	Val	Glu	His 680	Gln	Ser	Gln	Leu	Ile 685	Val	Arg	Val
Pro	Pro 690	Lys	Phe	Val	Val	Gln 695	Pro	Arg	Asp	Gln	Asp 700	Gly	Ile	Tyr	Gly
Lys 705	Ala	Val	Ile	Leu	Asn 710	Cys	Ser	Ala	Glu	Gly 715	Tyr	Pro	Val	Pro	Thr 720
Ile	Val	Trp	Lys	Phe 725	Ser	Lys	Gly	Ala	Gly 730	Val	Pro	Gln	Phe	Gln 735	Pro
Ile	Ala	Leu	Asn 740	Gly	Arg	Ile	Gln	Val 745	Leu	Ser	Asn	Gly	Ser 750	Leu	Leu
Ile	Lys	His 755	Val	Val	Glu	Glu	Asp 760	Ser	Gly	Tyr	Tyr	Leu 765	Cys	Lys	Val
Ser	Asn	Asp 770	Val	Gly	Ala	Asp 775	Val	Ser	Lys	Ser	Met 780	Tyr	Leu	Thr	Val
Lys 785	Ile	Pro	Ala	Met	Ile 790	Thr	Ser	Tyr	Pro	Asn 795	Thr	Thr	Leu	Ala	Thr 800

Table 1. (continued)	
1	100
2	100
3	100
4	100
5	100
6	100
7	100
8	100
9	100
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72	100
73	100
74	100
75	100
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100	100

Leu Gly Glu Ile Lys Asn Ile Thr Thr Thr Gln Pro Ser Leu Glu Leu
 1140 1145 1150
 Asp Gly Leu Glu Lys Tyr Thr Asn Tyr Ser Ile Gln Val Leu Ala Phe
 1155 1160 1165
 Thr Arg Ala Gly Asp Gly Val Arg Ser Glu Gln Ile Phe Thr Arg Thr
 1170 1175 1180
 Lys Glu Asp Val Pro Gly Pro Pro Ala Gly Val Lys Ala Ala Ala Ala
 1185 1190 1195 1200
 Ser Ala Ser Met Val Phe Val Ser Trp Leu Pro Pro Leu Lys Leu Asn
 1205 1210 1215
 Gly Ile Ile Arg Lys Tyr Thr Val Phe Cys Ser His Pro Tyr Pro Thr
 1220 1225 1230
 Val Ile Ser Glu Phe Glu Ala Ser Pro Asp Ser Phe Ser Tyr Arg Ile
 1235 1240 1245
 Pro Asn Leu Ser Arg Asn Arg Gln Tyr Ser Val Trp Val Val Ala Val
 1250 1255 1260
 Thr Ser Ala Gly Arg Gly Asn Ser Ser Glu Ile Ile Thr Val Glu Pro
 1265 1270 1275 1280
 Leu Ala Lys Ala Pro Ala Arg Ile Leu Thr Phe Ser Gly Thr Val Thr
 1285 1290 1295
 Thr Pro Trp Met Lys Asp Ile Val Leu Pro Cys Lys Ala Val Gly Asp
 1300 1305 1310
 Pro Ser Pro Ala Val Lys Trp Met Lys Asp Ser Asn Gly Thr Pro Ser
 1315 1320 1325
 Leu Val Thr Ile Asp Gly Arg Arg Ser Ile Phe Ser Asn Gly Ser Phe
 1330 1335 1340
 Ile Ile Arg Thr Val Lys Ala Glu Asp Ser Gly Tyr Tyr Ser Cys Ile
 1345 1350 1355 1360
 Ala Asn Asn Asn Trp Gly Ser Asp Glu Ile Ile Leu Asn Leu Gln Val
 1365 1370 1375
 Gln Val Pro Pro Asp Gln Pro Arg Leu Thr Val Ser Lys Thr Thr Ser
 1380 1385 1390
 Ser Ser Ile Thr Leu Ser Trp Leu Pro Gly Asp Asn Gly Gly Ser Ser
 1395 1400 1405
 Ile Arg Gly Tyr Ile Leu Gln Tyr Ser Glu Asp Asn Ser Glu Gln Trp
 1410 1415 1420
 Gly Ser Phe Pro Ile Ser Pro Ser Glu Arg Ser Tyr Arg Leu Glu Asn
 1425 1430 1435 1440
 Leu Lys Cys Gly Thr Trp Tyr Lys Phe Thr Leu Thr Ala Gln Asn Gly
 1445 1450 1455
 Val Gly Pro Gly Arg Ile Ser Glu Ile Ile Glu Ala Lys Thr Leu Gly
 1460 1465 1470

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